

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/579,007
Source: TFWP
Date Processed by STIC: 05/19/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 05/19/2006

PATENT APPLICATION: US/10/579,007

TIME: 08:26:03

Input Set : A:\795336PC.APP

Output Set: N:\CRF4\05192006\J579007.raw

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3 <110> APPLICANT: THERION BIOLOGICS CORPORATION
4     THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
5     REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF
6     HEALTH AND HUMAN SERVICES
8 <120> TITLE OF INVENTION: SYSTEM FOR TREATING AND PREVENTING BREAST CANCER
10 <130> FILE REFERENCE: 700953-53661-PCT
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/579,007
C--> 13 <141> CURRENT FILING DATE: 2006-05-11
15 <160> NUMBER OF SEQ ID NOS: 6
17 <170> SOFTWARE: PatentIn Ver. 3.3
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1548
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
26     nucleotide construct
28 <400> SEQUENCE: 1
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30 gttacgggtt ctggtcatgc aaagctctacc ccagggtggag aaaaggagac ttcggctacc 120
31 cagagaagtt cagtgccag ctctactgag aagaatgctg tgagtatgac aaagctccgta 180
32 ctctccagcc acagccccgg ttcaggctcc tccaccactc agggacagga tgtcactctg 240
33 gccccggcca cggaaccagc ttcaggttca gctgccttgt ggggacagga tgtcacctcg 300
34 gtaccagtta ctagaccagc tttaggtagc acagcacctc ctgctcatgg agtaactagt 360
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36 gcacctgata caagacctgc acctggatct acagcgccgc ctgcgcacgg agtgacatcg 480
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38 gcacccagata cccggccggc acccggaagt accgctccac ctgcacacgg ggtcacaagc 600
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41 gctaccacaa cccagccag caagagcact ccatttctca tcccagcca ccactctgat 780
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43 acggtacctc ctctcacctc ctccaatcac agcacttctc cccagttgtc tactgggggtc 900
44 tctttctttt tcctgtcttt tcacatttca aacctccagt ttaattcctc tctggaagat 960
45 cccagcacgg actactacca agagctgcag agagacattt ctgaaatgtt tttgcagatt 1020
46 tataaacaag ggggttttct gggcctctcc aatattaagt tcaggccagg atctgtggtg 1080
47 gtacaattga ctctggcctt ccgagaaggt accatcaatg tccacgacgt ggagacacag 1140
48 ttcaatcagt ataaaacgga agcagcctct cgatataacc tgacgatctc agacgtcagc 1200
49 gtgagtgatg tgccatttcc tttctctgcc cagtctgggg ctgggggtgcc aggctggggc 1260
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52 gatacctacc atcctatgag cgagtacccc acctaccaca cccatgggag ctatgtgccc 1440
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60 <211> LENGTH: 515
61 <212> TYPE: PRT
62 <213> ORGANISM: Artificial Sequence
64 <220> FEATURE:
65 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
66     protein construct
68 <400> SEQUENCE: 2
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70   1           5           10           15
72 Val Leu Thr Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
73           20           25           30
75 Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
76   35           40           45
78 Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
79   50           55           60
81 Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
82  65           70           75           80
84 Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Leu Trp Gly Gln
85           85           90           95
87 Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Ala
88   100          105          110
90 Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
91   115          120          125
93 Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
94   130          135          140
96 Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
97 145          150          155          160
99 Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
100 165          170          175
102 Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
103 180          185          190
105 Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
106 195          200          205
108 Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
109 210          215          220
111 Arg Pro Ala Pro Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg
112 225          230          235          240
114 Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser
115 245          250          255
117 His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr
118 260          265          270
120 Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser
121 275          280          285
123 Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe
124 290          295          300
126 Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp
127 305          310          315          320

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129 Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met
130           325           330           335
132 Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile
133           340           345           350
135 Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg
136           355           360           365
138 Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr
139           370           375           380
141 Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser
142 385           390           395           400
144 Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly Val
145           405           410           415
147 Pro Gly Trp Gly Ile Ala Leu Leu Val Leu Val Cys Val Leu Val Ala
148           420           425           430
150 Leu Ala Ile Val Tyr Leu Ile Ala Leu Ala Val Cys Gln Cys Arg Arg
151           435           440           445
153 Lys Asn Tyr Gly Gln Leu Asp Ile Phe Pro Ala Arg Asp Thr Tyr His
154           450           455           460
156 Pro Met Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg Tyr Val Pro
157 465           470           475           480
159 Pro Ser Ser Thr Asp Arg Ser Pro Tyr Glu Lys Val Ser Ala Gly Asn
160           485           490           495
162 Gly Gly Ser Ser Leu Ser Tyr Thr Asn Pro Ala Val Ala Ala Thr Ser
163           500           505           510
165 Ala Asn Leu
166           515
169 <210> SEQ ID NO: 3
170 <211> LENGTH: 2106
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial Sequence
175 <220> FEATURE:
176 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
177     nucleotide construct
179 <400> SEQUENCE: 3
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181 acagcctcac ttctaacctt ctggaaccgc cccaccactg ccaagctcac tattgaatcc 120
182 acgccgttca atgtgcgaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
183 catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
184 ggatatgtaa taggaactca acaagctacc ccagggccccg catacagtgg tcgagagata 300
185 atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360
186 accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta 420
187 tacccggaac tccctaagcc ttctattagc tccaataata gtaagcctgt cgaagacaaa 480
188 gatgccgtcg cttttacatg cgagcccgaa actcaagacg caacatatct ctgggtgggtg 540
189 aacaaccagt ccctgctgtg gtcccctaga ctccaactca gcaacggaaa tagaactctg 600
190 accctgttta acgtgaccag gaacgacaca gcaagctaca aatgcgaaac ccaaaatcca 660
191 gtcagcgcca ggaggtctga ttcagtgtat ctcaacgtgc tttacggacc cgatgtctct 720
192 acaatcagcc ctctaacac aagctataga tcaggggaaa atctgaatct gagctgtcat 780
193 gccgctagca atcctccgc ccaatacagc tgggttgtca atggcacttt ccaacagtcc 840
194 acccaggaac tgttcattcc caatattacc gtgaacaata gtggatccta cacgtgccaa 900

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195 gctcacaata ggcacaccgg actcaaccgc acaaccgtga cgacgattac cgtgtatgag 960
196 ccaccaaacc cattcataac tagtaacaat tctaaccagc ttgaggatga ggacgcagtt 1020
197 gcattaactt gtgagccaga gattcaaaat accacttatt tatggtgggt caataaccaa 1080
198 agtttgccgg ttagcccacg cttgcagttg tctaatagata accgcacatt gacactcctg 1140
199 tccgttactc gcaatgatgt aggaccttat gagtgtggca ttcagaatga attatccgtt 1200
200 gatcactccg accctgttat ccttaatgtt ttgtatggcc cagacgaccc aactatatct 1260
201 ccatcataca cctactaccg tcccggcggtg aacttgagcc tttcttgcca tgcagcatcc 1320
202 aacccccctg cacagtactc ctggctgatt gatggaaaca ttcagcagca tactcaagag 1380
203 ttattttataa gcaacataac tgagaagaac agcggactct atacttgcca ggccaataac 1440
204 tcagccagtg gtcacagcag gactacagtt aaaacaataa ctgtttccgc ggagctgccc 1500
205 aagccctcca tctccagcaa caactccaaa cccgtggagg acaaggatgc tgtggccttc 1560
206 acctgtgaac ctgaggctca gaacacaacc tacctgtggt gggtaaattg tcagagcctc 1620
207 ccagtcagtc ccaggctgca gctgtccaat ggcaacagga cctcactct attcaatgtc 1680
208 acaagaaatg acgcaagagc ctatgtatgt ggaatccaga actcagtgag tgcaaaccgc 1740
209 agtgaccagc tcacctgga tgtcctctat gggccggaca ccccatcat tccccccca 1800
210 gactcgtctt acctttcggg agcggacctc aacctctcct gccactcggc ctctaaccaca 1860
211 tccccgcagt attcttggcg tatcaatggg ataccgcagc aacacacaca agttctcttt 1920
212 atcgccaaaa tcacgccaaa taataacggg acctatgcct gttttgtctc taacttggct 1980
213 actggccgca ataattccat agtcaagagc atcacagtct ctgcatctgg aacttctcct 2040
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215 atatag 2106

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218 <210> SEQ ID NO: 4

219 <211> LENGTH: 372

220 <212> TYPE: PRT

221 <213> ORGANISM: Artificial Sequence

223 <220> FEATURE:

224 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 225 protein construct

227 <400> SEQUENCE: 4

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232 20 25 30
234 Leu Pro Val Ser Pro Arg Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu
235 35 40 45
237 Thr Leu Leu Ser Val Thr Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly
238 50 55 60
240 Ile Gln Asn Glu Leu Ser Val Asp His Ser Asp Pro Val Ile Leu Asn
241 65 70 75 80
243 Val Leu Tyr Gly Pro Asp Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr
244 85 90 95
246 Tyr Arg Pro Gly Val Asn Leu Ser Leu Ser Cys His Ala Ala Ser Asn
247 100 105 110
249 Pro Pro Ala Gln Tyr Ser Trp Leu Ile Asp Gly Asn Ile Gln Gln His
250 115 120 125
252 Thr Gln Glu Leu Phe Ile Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu
253 130 135 140
255 Tyr Thr Cys Gln Ala Asn Asn Ser Ala Ser Gly His Ser Arg Thr Thr
256 145 150 155 160

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258 Val Lys Thr Ile Thr Val Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser
259           165           170           175
261 Ser Asn Asn Ser Lys Pro Val Glu Asp Lys Asp Ala Val Ala Phe Thr
262           180           185           190
264 Cys Glu Pro Glu Ala Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly
265           195           200           205
267 Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg
268           210           215           220
270 Thr Leu Thr Leu Phe Asn Val Thr Arg Asn Asp Ala Arg Ala Tyr Val
271 225           230           235           240
273 Cys Gly Ile Gln Asn Ser Val Ser Ala Asn Arg Ser Asp Pro Val Thr
274           245           250           255
276 Leu Asp Val Leu Tyr Gly Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp
277           260           265           270
279 Ser Ser Tyr Leu Ser Gly Ala Asp Leu Asn Leu Ser Cys His Ser Ala
280           275           280           285
282 Ser Asn Pro Ser Pro Gln Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln
283           290           295           300
285 Gln His Thr Gln Val Leu Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn
286 305           310           315           320
288 Gly Thr Tyr Ala Cys Phe Val Ser Asn Leu Ala Thr Gly Arg Asn Asn
289           325           330           335
291 Ser Ile Val Lys Ser Ile Thr Val Ser Ala Ser Gly Thr Ser Pro Gly
292           340           345           350
294 Leu Ser Ala Gly Ala Thr Val Gly Ile Met Ile Gly Val Leu Val Gly
295           355           360           365
297 Val Ala Leu Ile
298           370
301 <210> SEQ ID NO: 5
302 <211> LENGTH: 31
303 <212> TYPE: DNA
304 <213> ORGANISM: Artificial Sequence
306 <220> FEATURE:
307 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
308     primer
310 <400> SEQUENCE: 5
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315 <211> LENGTH: 31
316 <212> TYPE: DNA
317 <213> ORGANISM: Artificial Sequence
319 <220> FEATURE:
320 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
321     primer
323 <400> SEQUENCE: 6
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VERIFICATION SUMMARY

DATE: 05/19/2006

PATENT APPLICATION: US/10/579,007

TIME: 08:26:04

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date